SEQUENCE LISTING

<110> Meyers, Rachel A. MacBeth, Kyle J. <120> 14094, A NOVEL TRYPSIN FAMILY MEMBER AND USES THEREFOR <130> 10448-046002 <150> US 09/633,300 <151> 2000-08-08 <150> US 60/200,621 <151> 2000-04-28 <160> 13 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 2948 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (628)...(1986) <221> misc_feature <222> (1)...(2948) <223> n = A, T, C or G<400> 1 aagagttqca tatcqcctcc catcaacaaa ctttccntqt atttccanac aatqtatttt 60 gtttgtcaaa tccagttttc ttgtaaacat tggggggtaa ataacagagg tggcttatga 120 gtatttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact 180 gttacccact ttgcctcgtc ttcaccctgt ccaaacaccg gtctccaatt tgcccttcaq 240 agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca 300 ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc 360 caaactccaa aaaaaaaccg gaattcagcc tggttaagtc caagctgaat tccgggtggg 420 ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattaggtc atgcccgtat 480 gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc 540 gtggtgccat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg 600 gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 654 Met Gly Glu Asn Asp Pro Pro Ala Val gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 702 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys 10 15 20 25 ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 750 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu

35

30

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						tcg Ser 160										1134
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						ttg Leu										1326
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gag aac Glu Asn 330				-	Trp 1	-					-	1662
aca gag Thr Glu												1710
cct ttg Pro Leu												1758
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340 345 350

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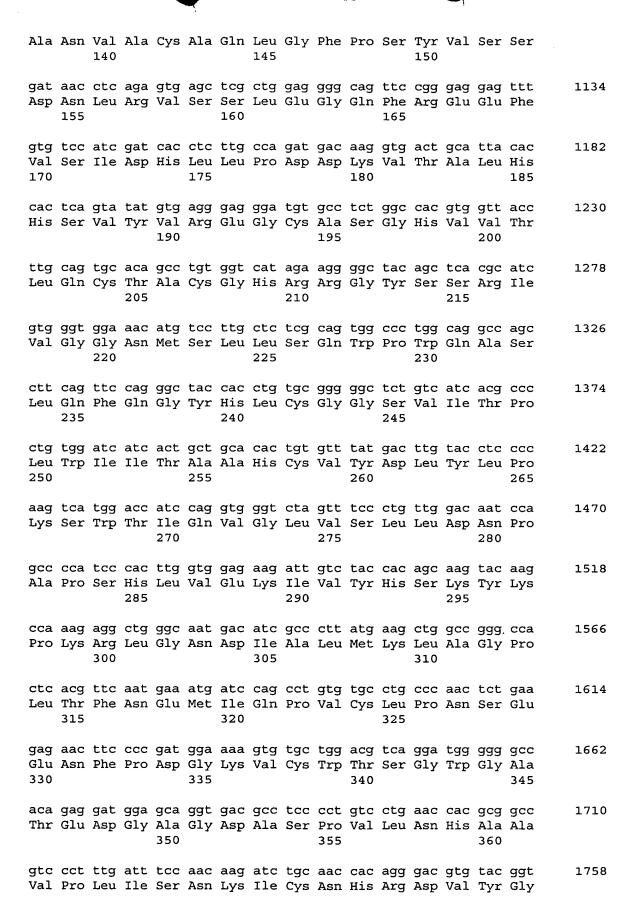
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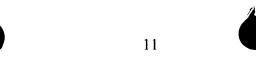
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Thr Glu Gln Lys Phe Asp Val Lys Lys Thr Ile Ile Val His Pro Asn
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Tyr Asn Pro Asp Thr Leu Asp Asn Gly Ala Tyr Asp Asn Asp Ile Ala
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Leu Leu Lys Leu Lys Ser Pro Gly Val Thr Leu Gly Asp Thr Val Arq
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Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp Leu Pro Val Gly Thr Thr
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Cys Thr Val Ser Gly Trp Gly Arg Pro Thr Lys Asn Leu Gly Leu
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Cys Arg Ser Ala Tyr Glu Tyr Gly Gly Thr Asp Asp Lys Val Glu Phe
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Val Thr Asp Asn Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala
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Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Asn Arg
                        215
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Asp Gly Arg Trp Glu Leu Val Gly Ile Val Ser Trp Gly Ser Tyr Gly
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Cys Ala Arg Gly Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr
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Val Ile Lys Val Ser Lys Ile Ile Glu Val His Pro Asn Tyr Asn Asn
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Cys Arg Met Leu Cys Ala Gly Tyr Leu Glu Gly Gly Asn Thr Pro Gly
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Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Val
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Gly Gly Ala Val Ser Leu Leu Gly Pro Tyr Phe Ser Glu Gly Gly
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Pro Ala Gly Gln Arg Glu Ile Trp Leu Asp Gly Val Asn Cys Ser Gly
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Asn Glu Thr Ser Leu Ser Gln Cys Pro Val Arg Val Thr Pro Pro Gly
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Ser
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